

SEQUENCE LISTING

<110> LINDNER, Volkhard  
FRIESEL, Robert F.

<120> COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL

<130> 36-13 Lindner et al. (200036.0013)

<140> Not Yet Assigned

<141> 2000-10-19

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1192

<212> DNA

<213> Rattus sp.

<400> 1

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ccgtccagcg cctctgagaa tcccaaggtg aagcaaaaag cgctgtatccg gcagagggaa 240  
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<210> 2

<211> 245

<212> PRT

<213> Rattus sp.

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 Phe Leu Val Leu Leu Leu Leu Gln Leu Ser Ala Pro Ser Ser Ala  
 20 25 30  
  
 Ser Glu Asn Pro Lys Val Lys Gln Lys Ala Leu Ile Arg Gln Arg Glu  
 35 40 45  
  
 Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val  
 50 55 60  
  
 Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro  
 65 70 75 80  
  
 Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu  
 85 90 95  
  
 Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser  
 100 105 110  
  
 Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys  
 115 120 125  
  
 Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser  
 130 135 140  
  
 Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr  
 145 150 155 160  
  
 Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala  
 165 170 175  
  
 Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Leu Asn Ser Thr Ile Asn  
 180 185 190  
  
 Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala  
 195 200 205  
  
 Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro  
 210 215 220  
  
 Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile  
 225 230 235 240  
  
 Glu Glu Leu Pro Lys

<210> 3  
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 <212> DNA  
 <213> Homo sapiens

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<210> 4  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
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 1 5 10 15

Leu	Leu	Leu	Leu
Leu	Leu	Leu	Leu

Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu  
 20 25 30

Ile	Pro	Lys	Gly
Lys	Gln	Lys	Ala

Gln Leu Arg Gln Arg Glu Val Val  
 35 40 45

Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly

50	55	60
Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile		
65	70	75
Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu		
85	90	95
Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser		
100	105	110
Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe		
115	120	125
Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser		
130	135	140
Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr		
145	150	155
Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile		
165	170	175
Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His		
180	185	190
Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu		
195	200	205
Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly		
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Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu		
225	230	235
Leu Pro Lys		

<210> 5  
 <211> 277  
 <212> PRT  
 <213> Rattus sp.

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20 25 30

Met His Pro Gln Gly Arg Ala Ala Ser Pro Gln Leu Leu Leu Gly Leu  
35 40 45

Phe Leu Val Leu Leu Leu Leu Gln Leu Ser Ala Pro Ser Ser Ala  
50 55 60

Ser Glu Asn Pro Lys Val Lys Gln Lys Ala Leu Ile Arg Gln Arg Glu  
65 70 75 80

Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val  
85 90 95

Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro  
100 105 110

Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu  
115 120 125

Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser  
130 135 140

Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys  
145 150 155 160

Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser  
165 170 175

Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr  
180 185 190

Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala  
195 200 205

Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Leu Asn Ser Thr Ile Asn  
210 215 220

Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala  
225 230 235 240

Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro  
245 250 255

Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile  
260 265 270

Glu Glu Leu Pro Lys

275

<210> 6

<211> 403

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:REMODEL  
antisense ribonucleoprobe

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gucuaccagu ccagcaccaa ucccuucaca gaguccuucc acggaggaag uacgaugaau 120  
auuaauaguu gaauuuuacu cagggcuucc uugguccaga uagaugauag cuucaauggg 180  
aagagguccu gaacauucag cuccauuaaa gguaaaaauac cagcguugac agcaagcauu 240  
ccugcauuug agccgaagcg agccacugaa cagaacucga agagcgcugu uggaucgc当地 300  
cuuugugaaau guacauuccg caauuuuuccc aagaucuaug ccauaauuaa gugaacucca 360  
ugaacacugc uuguaguuug ggguccagga uuccucaaag cuu 403

<210> 7

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial  
Sequence:carboxy-terminal amino acids of REMODEL

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Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu Leu Pro Lys

1

5

10

15

<210> 8

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:insulin signal  
peptide

<400> 8

Met Ala Leu Leu Val His Phe Leu Pro Leu Leu Ala Leu Leu Ala Leu

1

5

10

15

Trp Glu Pro Lys Pro Thr Gln Ala  
20

<210> 9  
<211> 734  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:myc-tagged  
REMODEL construct

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aagcgctgtat ccggcagagg gaagtggtag acctgtataa tggatgtgc ctacaaggac 180  
cagcaggagt tcctggtcgc gatgggagcc ctggggccaa tggcatctt ggcacaccgg 240  
gaatcccagg tcgggatgga ttcaaaggag agaaaaggga gtgcttaagg gaaagctttg 300  
aggaatcctg gacccaaac tacaagcagt gttcatggag ttcacttaat tatggcatag 360  
atcttggaa aattgcggaa tgtacattca caaagatgct atccaaacagc gotcttcgag 420  
ttctgttcag tggctcgctt cggtctaaat gcaggaatgc ttgctgtcaa cgctggatt 480  
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gactctgtga agggatttgt gctggactgg tagacgtggc catctgggtc ggcacctgtt 660  
cagattaccc caaaggagac gcttctactg ggtgaaattc tgtgtccgc atcatcattg 720  
aagaactacc aaaa 734